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**THE ITALIAN CONTRIBUTION TO THE INTERNATIONAL SOLANACEAE GENOME PROJECT (SOL)**

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In November 2003 the International Solanaceae Genome Project (SOL) was launched, with the long-term goal of developing the Solanaceae family as a model for applying a systems approach to plant adaptation and diversification (<http://www.sgn.cornell.edu/>). Over the coming decade SOL will integrate diverse disciplines and research groups from around the world to create a coordinated network of knowledge about the Solanaceae family and related taxa.

The first goal of SOL is to obtain a high quality sequence of the tomato genome as a reference for the entire project. Tomato (*Solanum lycopersicum*) is the model plant for the Solanaceae family: it provides the smallest diploid genome for which homozygous inbreds are available, and it is the most intensively studied Solanaceae genome. The availability of a reference genome for the Solanaceae will enhance the possibility for map-based gene cloning and marker-assisted breeding within this family and will benefit enormously studies on comparative genomics, taxonomy, and post genomics in many fields.

The tomato genome contains 950 Mb of DNA organized into 12 chromosomes ( $n=x=12$ ), the distal portions of which are comprised of largely continuous stretches of gene-rich euchromatin which corresponds to less than 25% (220~250 Mb) of the total DNA in the tomato nucleus. The sequencing of the tomato euchromatin is being pursued by an International Consortium of ten countries from around the world, and it is being accomplished on a BAC by BAC basis with the purpose of obtaining a minimal tiling path anchored to the high density EST map. Each country has taken responsibility for sequencing specific chromosomes while developing suitable bioinformatic platforms. Italy is sequencing tomato chromosome 12, for which 11 Mb of euchromatin have been estimated. The Italian sequencing initiative is supported by grants from the Italian Ministry of Agriculture (MiPAF), AGRO-NANOTECH Project, and by the Italian Ministry of Research (MIUR), FIRB (Laboratories) Project. To date 22 seed BACs (BACs that have been anchored to the tomato EST map) associated to 17 markers mapping on chromosome 12 have been selected for validation and sequencing. The map position of the clones is being confirmed by means of SNPs identified on the *S. pennellii* IL population. Sequencing has been completed to Phase 3 for three seed BACs and the SGN BAC-end database has been screened by BLASTN in order to identify

new BACs to move out of the three finished seed BACs ensuring a minimum overlap. A total of 22 BACs are currently at different phases of the sequencing pipeline. A program complementary to the SGN Online BLAST Interface, is being developed to allow a more efficient choice of overlapping BAC clones. In addition, a bioinformatic platform has been built to provide an Italian resource to support the experimental annotation of the tomato genome.